

<!--StartFragment-->RESULT 3

ABA94700

ID ABA94700 standard; cDNA; 3197 BP.

XX

AC ABA94700;

XX

DT 23-APR-2002 (first entry)

XX

DE Human lipid metabolism molecule (LMM) cDNA (ID: 7477093CB1).

XX

KW Lipid metabolism molecule; LMM; cytostatic; nootropic; neuroprotective;
KW anticonvulsant; immunosuppressive; anti-inflammatory; dermatological;
KW cardiovascular; antiHIV; antiemetic; antiallergic; hypertensive; human;
KW cancer; gene therapy; protein therapy; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..3081

FT /*tag= a

FT /product= "LMM"

XX

PN WO200204490-A2.

XX

PD 17-JAN-2002.

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PF 06-JUL-2001; 2001WO-US021432.

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PR 07-JUL-2000; 2000US-0216801P.

PR 07-JUL-2000; 2000US-0216803P.

PR 14-JUL-2000; 2000US-0218233P.

PR 21-JUL-2000; 2000US-0220046P.

PR 26-JUL-2000; 2000US-0220739P.

PR 04-AUG-2000; 2000US-0222824P.

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PA (INCY-) INCYTE GENOMICS INC.

XX

PI Tang YT, Azimzai Y, Das D, Thornton M, Lu DAM, Tribouley CM;

PI Yue H, Gandhi AR, Walia NK, Khan FA, Lu Y, Yao MG, Hafalia AJA;

PI Elliott VS, Patterson C, Lal P, Ramkumar J, Nguyen DB, Baugn MR;

XX

DR WPI; 2002-164631/21.

DR P-PSDB; ABB07497.

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PT Lipid metabolism molecules useful in diagnosing, treating or preventing
PT cancers, and neurological, autoimmune/inflammatory, gastrointestinal,
PT skin and cardiovascular disorders.

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PS Claim 5; Page 126-127; 128pp; English.

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CC The invention provides human lipid metabolism molecule (LMM) polypeptides
CC and polynucleotides. The LMM polypeptides can be expressed by standard
CC recombinant methodology. The LMM polypeptides are useful for diagnosing
CC or treating a condition or disease associated with the expression of LMM,
CC or screening for compounds that specifically bind to or modulate the
CC activity or expression of LMM. They are also used to generate antibodies
CC and assess the toxicity of test compounds. The LMM polypeptides,
CC modulators and antibodies are specifically useful for diagnosing,
CC treating or preventing cancers (e.g. adenocarcinoma, leukemia, lymphoma,
CC melanoma or sarcoma), neurological disorders (e.g. epilepsy, stroke,
CC cerebral neoplasms, Alzheimer's disease or Pick's disease), autoimmune/

SEQ ID NO: 8

alignment

Does not encode SEQ ID NO: 9

CC inflammatory disorders (e.g. AIDS, Addison's disease, allergies, asthma,
 CC or atherosclerosis), gastrointestinal disorders (e.g. dysphagia, peptide
 CC esophagitis, gastritis, gastric carcinoma, anorexia or nausea), skin
 CC disorders (e.g. dermatitis, eczema, or scleroderma), and cardiovascular
 CC disorders (e.g. hypertension, arterial dissections, vascular tumours, or
 CC thrombolysis). The present sequence represents a human LMM polynucleotide
 CC sequence
 XX

SQ Sequence 3197 BP; 644 A; 994 C; 951 G; 608 T; 0 U; 0 Other;

Query Match 73.2%; Score 2627.4; DB 6; Length 3197;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 2663; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

Qy	8	GTCCTATCCCACTGGGACCGTCGCTGCCACTCAGCCAGAGAGCCAGCATCTTGGCAAGGG	67
Db	509	GTCCTATCCCACTGGGACCGTCGCTGCCACTCAGCCAGAGAGCCAGCATCTTGGCAAGGG	568
Qy	68	CTGGGCTGGAGTGAAGCTGGAAGGGCTAGCATGGAGAGCCGTGACCTGGGGGACCAAC	127
Db	569	CTGGGCTGGAGTGAAGCTGGAAGGGCTAGCATGGAGAGCCGTGACCTGGGGGACCAAC	628
Qy	128	TGGCCACCCCTTACCA-----GAGGGAGGCTCTACCTGCT	162
Db	629	TGGCCACCCCTTACCAAGGCGCCAGTGCCAGCAGACGACAGGGGGGAGGCTCTACCTGCT	688
Qy	163	GGCAGCTCACAGTGAGGGTCCTGGAGGCGCGGAACCTGCGCTGGGCTGACCTGTTGAGTG	222
Db	689	GGCAGCTCACAGTGAGGGTCCTGGAGGCGCGGAACCTGCGCTGGGCTGACCTGTTGAGTG	748
Qy	223	AGGCCGACCCCTTACGTGATCCTACAGCTGTGACCCACCTGGAATGAAGTTTAAAGACA	282
Db	749	AGGCCGACCCCTTACGTGATCCTACAGCTGTGACCCACCTGGAATGAAGTTTAAAGACA	808
Qy	283	AGACGCTCACCGACACCAGTCATCCTGTGTGGAATGAGGCTTCCGTTTCCTTATCCAAA	342
Db	809	AGACGCTCACCGACACCAGTCATCCTGTGTGGAATGAGGCTTCCGTTTCCTTATCCAAA	868
Qy	343	GTCAGGTCAAGAATGTTCTGGAGCTTAGCATCTATGATGAGGACTCAGTCACGGAGGATG	402
Db	869	GTCAGGTCAAGAATGTTCTGGAGCTTAGCATCTATGATGAGGACTCAGTCACGGAGGATG	928
Qy	403	ACATCTGCTTCAAGGTTCTCTATGACATCTCAGAAGTCTCCCTGGCAAGCTGCTCCGGA	462
Db	929	ACATCTGCTTCAAGGTTCTCTATGACATCTCAGAAGTCTCCCTGGCAAGCTGCTCCGGA	988
Qy	463	AAACCTTCTCCAGAGTCCCGAGGAGAGGAGCTGGATGTGGAGTTCTCTGATGGAAG	522
Db	989	AAACCTTCTCCAGAGTCCCGAGGAGAGGAGCTGGATGTGGAGTTCTCTGATGGAAG	1048
Qy	523	AAACGTCAGATCGCCAGAAAACCTCATCACAACAAAGTCATTGTGGCCGAGAGCTGT	582
Db	1049	AAACGTCAGATCGCCAGAAAACCTCATCACAACAAAGTCATTGTGGCCGAGAGCTGT	1108
Qy	583	CATGCTGGATGTGCATCTGGACAGCACAGGAGCACCGCTGTGGTTGCAGATCAGGACA	642
Db	1109	CATGCTGGATGTGCATCTGGACAGCACAGGAGCACCGCTGTGGTTGCAGATCAGGACA	1168
Qy	643	AGCTGGAGCTGGAGCTGGTGCTGAAGGGTCTATGAGGACACACAGACATCCTTCTCG	702
Db	1169	AGCTGGAGCTGGAGCTGGTGCTGAAGGGTCTATGAGGACACACAGACATCCTTCTCG	1228

Qy	703	GCACAGCCTCTGCCTTCCGCTTCCACTACATGGCAGCCCTAGAGACAGAGCTGAGCGGGC	762
Db	1229	GCACAGCCTCTGCCTTCCGCTTCCACTACATGGCAGCCCTAGAGACAGAGCTGAGCGGGC	1288
Qy	763	GCCTGAGGAGCTCCAGAAGCAATGGCTGGAATGGGACAACTCAGCTGGGTACCTCACTG	822
Db	1289	GCCTGAGGAGCTCCAGAAGCAATGGCTGGAATGGGACAACTCAGCTGGGTACCTCACTG	1348
Qy	823	TGCCCCTGAGGCCCTTGACCATTTGGGAAGGAGGTGACTATGGATGTTCTGCTCCAAATG	882
Db	1349	TGCCCCTGAGGCCCTTGACCATTTGGGAAGGAGGTGACTATGGATGTTCTGCTCCAAATG	1408
Qy	883	CCCCAGGAGTGAGGCTGCAGCTCAAGGCAGAGGGCTGCCCTGAGGAGCTGGCCGTGCACC	942
Db	1409	CCCCAGGAGTGAGGCTGCAGCTCAAGGCAGAGGGCTGCCCTGAGGAGCTGGCCGTGCACC	1468
Qy	943	TGGGCTTCAATCTCTGTGCAGAGGAGCAGGCCCTTCCTGAGCAGGAGGAAGCAGGTGGTGG	1002
Db	1469	TGGGCTTCAATCTCTGTGCAGAGGAGCAGGCCCTTCCTGAGCAGGAGGAAGCAGGTGGTGG	1528
Qy	1003	CCAAGGCCCTGAAGCAGGCCCTGCAGCTGGACAGAGACCTGCAGGAGGATGAGGTACCCG	1062
Db	1529	CCAAGGCCCTGAAGCAGGCCCTGCAGCTGGACAGAGACCTGCAGGAGGATGAGGTACCCG	1588
Qy	1063	TTGTGGGCATCATGGCCACAGGAGGAGTGCCCGGGCCATGACCTCACTCTACGGCCACC	1122
Db	1589	TTGTGGGCATCATGGCCACAGGAGGAGTGCCCGGGCCATGACCTCACTCTACGGCCACC	1648
Qy	1123	TATTGGCCTTGCAAGCTGGGCCCTCTAGACTGTGTGACCTACTTCACTGGCATCTCTG	1182
Db	1649	TATTGGCCTTGCAAGCTGGGCCCTCTAGACTGTGTGACCTACTTCACTGGCATCTCTG	1708
Qy	1183	GCTCTACGTGGACAATGGGCCACCTGTACGGGACCTGAGTGGTCGACAGGGACCTGG	1242
Db	1709	GCTCTACGTGGACAATGGGCCACCTGTACGGGACCTGAGTGGTCGACAGGGACCTGG	1768
Qy	1243	AGGGACCTATCAGATACGCCCGGGAGCACCTGGCCAAGAGCAAGCTGGAGGTCTTTTCCC	1302
Db	1769	AGGGACCTATCAGATACGCCCGGGAGCACCTGGCCAAGAGCAAGCTGGAGGTCTTTTCCC	1828
Qy	1303	CAGAGCGCTTGGCGAGCTACCGCCGGGAGCTGGAGCTGCGGGCTGAGCAGGGCCACCCCA	1362
Db	1829	CAGAGCGCTTGGCGAGCTACCGCCGGGAGCTGGAGCTGCGGGCTGAGCAGGGCCACCCCA	1888
Qy	1363	CGACCTTTGTGGACCTGTGGGCGCTAGTGTGGAGTCCATGCTGCACGGCCAGGTGATGG	1422
Db	1889	CGACCTTTGTGGACCTGTGGGCGCTAGTGTGGAGTCCATGCTGCACGGCCAGGTGATGG	1948
Qy	1423	ATCAGAAGCTGTGAGGACAGAGAGCCGCCCTGGAACGGGGTCAAGACCTCTGCCCTCT	1482
Db	1949	ATCAGAAGCTGTGAGGACAGAGAGCCGCCCTGGAACGGGGTCAAGACCTCTGCCCTCT	2008
Qy	1483	ACTTGAGCCTCAATGTCAAAGAGAAACAATCTGGAGACACTGGACTTCAAGGAGTGGGTG	1542
Db	2009	ACTTGAGCCTCAATGTCAAAGAGAAACAATCTGGAGACACTGGACTTCAAGGAGTGGGTG	2068
Qy	1543	AGTTCTCCCCCTATGAGGTCGGTTTCTGAAGTACGGGGCTTCGTCCCTCTGAGCTCT	1602
Db	2069	AGTTCTCCCCCTATGAGGTCGGTTTCTGAAGTACGGGGCTTCGTCCCTCTGAGCTCT	2128

Qy	1603	TCGGCTCCGAGTCTTCATGGGACGGCTGATGAGGAGGATCCCGAGCCCCGGATCTGCT	1662
Db	2129	TCGGCTCCGAGTCTTCATGGGACGGCTGATGAGGAGGATCCCGAGCCCCGGATCTGCT	2188
Qy	1663	TTCTGGAAGCCATCTGGAGCAACATTTCTCCCTGAACCTGCTGGATGCTGGTATGACC	1722
Db	2189	TTCTGGAAGCCATCTGGAGCAACATTTCTCCCTGAACCTGCTGGATGCTGGTATGACC	2248
Qy	1723	TCACCACTTCTGGGGAGTCTCGGAAACAGCACATCAAGGACAAGACCAGGAGCTTAGAGA	1782
Db	2249	TCACCACTTCTGGGGAGTCTCGGAAACAGCACATCAAGGACAAGACCAGGAGCTTAGAGA	2308
Qy	1783	AGGAGCCCCCTGACCACCTCGGGGACCTCCTCGCGGCTGGAGGCCTCGTGGCTGCAGCCAG	1842
Db	2309	AGGAGCCCCCTGACCACCTCGGGGACCTCCTCGCGGCTGGAGGCCTCGTGGCTGCAGCCAG	2368
Qy	1843	GCACGGCGCTGGCCAGGCATTAAAGGCTTCCTGACAGGCAGGCCCTCCACCAGCGCA	1902
Db	2369	GCACGGCGCTGGCCAGGCATTAAAGGCTTCCTGACAGGCAGGCCCTCCACCAGCGCA	2428
Qy	1903	GCCCCAACTTCTCCAGGGCCTCCAGCTGCACCAGGACTACTGTAGCCACAAGACTTCT	1962
Db	2429	GCCCCAACTTCTCCAGGGCCTCCAGCTGCACCAGGACTACTGTAGCCACAAGACTTCT	2488
Qy	1963	CCACCTGGGCAGACTACCAGCTTGACTCCATGCCAGCCAGCTGACCCCCAAGGAGCCCC	2022
Db	2489	CCACCTGGGCAGACTACCAGCTTGACTCCATGCCAGCCAGCTGACCCCCAAGGAGCCCC	2548
Qy	2023	GGCTCTGCCTGGTGGACGCCCTACTTCATCAACACCAGCTCTCCCTCCATGTTCCGGC	2082
Db	2549	GGCTCTGCCTGGTGGACGCCCTACTTCATCAACACCAGCTCTCCCTCCATGTTCCGGC	2608
Qy	2083	CAGGCCGAGGCTGGACCTCATCTCTCCTTCGACTACTCCCTATCTGCGCCCTTCGAGG	2142
Db	2609	CAGGCCGAGGCTGGACCTCATCTCTCCTTCGACTACTCCCTATCTGCGCCCTTCGAGG	2668
Qy	2143	CACTGCAGCAGACGGAGCTGTACTGCCGGCCCCGGGGGTGCCCTTCCCCGGGTGGAAC	2202
Db	2669	CACTGCAGCAGACGGAGCTGTACTGCCGGCCCCGGGGGTGCCCTTCCCCGGGTGGAAC	2728
Qy	2203	CCAGCCCTCAGGACCAGCACCAGCCAAGGGAATGCCACCTCTTCTCAGACCCCGCTGCC	2262
Db	2729	CCAGCCCTCAGGACCAGCACCAGCCAAGGGAATGCCACCTCTTCTCAGACCCCGCTGCC	2788
Qy	2263	CCGAGGCCCGGATCTGCTGCACTTCCCGTGGTCAATGCCCTCTTCAAGGACCCTCAG	2322
Db	2789	CCGAGGCCCGGATCTGCTGCACTTCCCGTGGTCAATGCCCTCTTCAAGGACCCTCAG	2848
Qy	2323	CCCCGGTGTCCAGCGCAGCCCCGAGAGCTCCAGGGTGGCCAAGTGGATCTCACCGGGG	2382
Db	2849	CCCCGGTGTCCAGCGCAGCCCCGAGAGCTCCAGGGTGGCCAAGTGGATCTCACCGGGG	2908
Qy	2383	CCACCTGCCCCACACCTGTCCAACATGACCTACAAGGAGGAAGACTTCAGAGCGCTGC	2442
Db	2909	CCACCTGCCCCACACCTGTCCAACATGACCTACAAGGAGGAAGACTTCAGAGCGCTGC	2968
Qy	2443	TGCGGCTCAGTGACTACAACGTGCAGACCAGCCAGGGTGCCATCTCGCAGGCCCTGAGGA	2502
Db	2969	TGCGGCTCAGTGACTACAACGTGCAGACCAGCCAGGGTGCCATCTCGCAGGCCCTGAGGA	3028
Qy	2503	CCGCGCTGAAGCACCGGACTCTAGAGGCGAGGCTCCAAGGGCACAGACCTGAGGTGCT	2562

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Db      3029  CCGCGCTGAAGCACCGGACTCTAGAGGCGAGGCCTCCAAGGGCACAGACCTGAGTTGCT 3088
Qy      2563  CAGAGGCTGCAGGACCTCCAGGGCCTGCGGGCATAACCTGATCTGTAGCTGGGCTCAGC 2622
Db      3089  CAGAGGCTGCAGGACCTCCAGGGCCTGCGGGCATAACCTGATCTGTAGCTGGGCTCAGC 3148
Qy      2623  CACAGGCCTTCCTGGTTGGAGTTCTGGGCTCTCCCAGGCCTGGGTGGCC 2671
Db      3149  CACAGGCCTTCCTGGTTGGAGTTCTGGGCTCTCCCAGGCCTGGGTGGCC 3197
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